

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: July 11, 2004, 09:32:59 ; Search time 46 Seconds

(without alignments)  
108.493 Million cell updates/sec

Title: US-10-001-938-3  
Perfect score: 86  
Sequence: 1 QKRAAYDQYGHAFQ 16

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues

Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	16	14 US-10-001-938-3	Sequence 3, Appl1
2	86	100.0	340	9 US-09-764-868-1153	Sequence 1153, Ap
3	86	100.0	341	9 US-09-764-868-1152	Sequence 1152, Ap
4	86	100.0	376	15 US-10-369-493-689	Sequence 689, App
5	86	100.0	378	15 US-10-369-493-386	Sequence 386, App
6	86	100.0	378	15 US-10-369-493-21305	Sequence 21305, A
7	81	94.2	13	9 US-09-766-993-10	Sequence 10, Appl
8	81	94.2	15	9 US-09-828-574-10	Sequence 10, Appl
9	81	94.2	15	14 US-10-001-938-27	Sequence 27, Appl
10	81	94.2	15	14 US-10-299-540-4	Sequence 4, Appl1
11	81	94.2	15	14 US-10-299-184-4	Sequence 4, Appl1
12	81	94.2	15	14 US-10-239-313A-444	Sequence 444, App
13	81	94.2	15	14 US-10-239-313A-447	Sequence 447, App
14	79	91.9	365	15 US-10-369-493-10648	Sequence 10648, A
15	78	90.7	376	15 US-10-369-493-12087	Sequence 12087, A

16	72	83.7	15	9 US-09-828-574-11	Sequence 11, Appl
17	72	83.7	15	14 US-10-299-540-5	Sequence 5, Appl1
18	72	83.7	15	14 US-10-299-184-5	Sequence 5, Appl1
19	69	80.2	382	15 US-10-369-493-8065	Sequence 8065, Ap
20	69	80.2	384	15 US-10-369-493-21849	Sequence 21849, A
21	67	77.9	379	15 US-10-369-493-7330	Sequence 7330, Ap
22	67	77.9	380	15 US-10-369-493-4573	Sequence 4573, Ap
23	63	73.3	376	15 US-10-369-493-4573	Sequence 47, Appl
24	62	72.1	374	15 US-10-369-493-13658	Sequence 13658, A
25	61	70.9	378	15 US-10-369-493-8450	Sequence 8450, Ap
26	60	69.8	368	9 US-09-861-451A-2	Sequence 2, Appl1
27	60	69.8	375	15 US-10-369-493-15859	Sequence 15859, A
28	60	69.8	376	15 US-10-369-493-15487	Sequence 15487, A
29	59	68.6	358	15 US-10-369-493-9641	Sequence 9641, Ap
30	58	67.4	379	15 US-10-369-493-18523	Sequence 18523, A
31	58	67.4	385	15 US-10-369-493-16754	Sequence 16754, A
32	57	66.3	369	15 US-10-369-493-19646	Sequence 19646, A
33	56	65.1	362	15 US-10-369-493-9305	Sequence 9305, Ap
34	56	65.1	378	16 US-10-474-776-634	Sequence 634, App
35	54	62.8	15	14 US-10-299-540-6	Sequence 6, Appl1
36	54	62.8	15	14 US-10-299-184-6	Sequence 6, Appl1
37	53	61.6	423	15 US-10-369-493-12619	Sequence 12619, A
38	52	60.5	360	15 US-10-369-493-10371	Sequence 10371, A
39	52	60.5	372	15 US-10-369-493-23206	Sequence 23206, A
40	52	60.5	376	15 US-10-369-493-1212	Sequence 1212, Ap
41	50	58.1	297	12 US-10-282-122A-54551	Sequence 54551, A
42	50	58.1	362	12 US-10-437-963-190831	Sequence 190831, A
43	50	58.1	383	16 US-10-437-963-108162	Sequence 108162, A
44	50	58.1	404	12 US-10-425-114-59964	Sequence 59964, A
45	49	57.0	146	12 US-10-424-599-191916	Sequence 191916, A

## ALIGNMENTS

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US-10-001-938-3  
; Sequence 3, Application US/10001938  
; Publication No. US20030031679A1  
; GENERAL INFORMATION:  
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
; APPLICANT: ALBANI, Salvatore  
; APPLICANT: CARSON, Dennis  
; APPLICANT: PRAKREN, Berent  
; APPLICANT: MARTINI, Alberto  
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND USI  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: UCSD1360-1  
; CURRENT APPLICATION NUMBER: US/10/001,938  
; CURRENT FILING DATE: 2001-10-31  
; PRIOR APPLICATION NUMBER: US 60/245,181  
; PRIOR FILING DATE: 2000-11-01  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 16  
; TYPE: PRT  
; ORGANISM: Escherichia coli  
US-10-001-938-3  
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Best Local Similarity 100.0%; Pred. No. 9.3e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 QKRAAYDQYGHAFQ 16  
RESULT 2  
US-09-764-868-1153  
; Sequence 1153, Application US/09764868  
; Patent No. US20020168711A1

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1153
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (110)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (135)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (156)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (196)
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; NAME/KEY: SITE
; LOCATION: (198)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; LOCATION: (216)
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; US-09-764-868-1153

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RESULT 3
; US-09-764-868-1152
; Sequence 1152, Application US/09764868
; Patent No. US20020168711A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT232
; CURRENT APPLICATION NUMBER: US/09/764,868
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1510
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1152
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-764-868-1152

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RESULT 4
US-10-369-493-689

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; Sequence 689, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 689
; LENGTH: 376
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-10-369-493-689

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Best Local Similarity 100.0%; Pred. No. 2.4e-06;
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RESULT 5
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; Sequence 386, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 386
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Xenorhabdus nematophilus
; US-10-369-493-386

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Query Match          100.0%; Score 86; DB 15; Length 378;
Best Local Similarity 100.0%; Pred. No. 2.4e-06;
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Db 61 QKRAAYDQYGHAAFEQ 76

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US-10-369-493-21305
; Sequence 21305, Application US/10369493
; Publication No. US2003023675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:30:33 ; Search time 23 Seconds  
(without alignments)  
35.914 Million cell updates/sec

Title: US-10-001-938-3  
Perfect score: 86  
Sequence: 1 OKRAAYDQGHAAFEQ 16

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Total number of hits satisfying chosen parameters: 389414

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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep: \*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	86	100.0	131	4	US-09-618-869-4
3	86	100.0	380	4	US-09-543-681A-5912
4	86	100.0	380	4	US-09-489-039A-9011
5	86	100.0	399	4	US-09-553-498-2
6	86	100.0	399	4	US-09-618-869-2
7	81	94.2	15	1	US-08-618-464-4
8	81	94.2	15	1	US-09-107-615-4
9	81	94.2	15	5	PCT-US95-04896-4
10	72	83.7	15	5	US-08-618-464-5
11	72	83.7	15	5	US-09-107-615-5
12	72	83.7	15	5	PCT-US95-04896-5
13	62	72.1	381	4	US-09-252-991A-71174
14	61	70.9	407	4	US-09-546-236-2899
15	56	66.1	352	2	US-08-472-534-6
16	54	62.8	15	1	US-08-618-464-6
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19	47	54.7	385	4	US-09-134-001C-3688
20	45	53.3	419	2	US-08-686-417-3
21	45	52.3	677	4	US-09-252-991A-18102
22	44	51.2	915	4	US-09-252-991A-44992
23	43	50.0	1895	2	US-08-619-554-4
24	41	47.7	87	4	US-09-882-835-4
25	41	47.7	87	4	US-09-658-644-4
26	41	47.7	348	2	US-08-974-546-1
27	41	47.7	387	4	US-09-543-681A-7130

28	41	47.7	845	4	US-09-252-991A-29230	Sequence 29230, A
29	40	46.5	317	4	US-09-328-352-8169	Sequence 8169, Ap
30	40	46.5	487	4	US-09-252-991A-21980	Sequence 21980, A
31	38	44.2	107	1	US-08-326-117B-3	Sequence 3, Appli
32	38	44.2	107	3	US-08-982-129-3	Sequence 3, Appli
33	38	44.2	108	3	US-08-893-534A-5	Sequence 5, Appli
34	38	44.2	108	3	US-08-996-679-5	Sequence 5, Appli
35	38	44.2	108	3	US-08-939-853A-7	Sequence 7, Appli
36	38	44.2	108	3	US-09-115-395-5	Sequence 5, Appli
37	38	44.2	108	3	US-09-113-977C-38	Sequence 38, Appli
38	38	44.2	108	4	US-09-507-102-5	Sequence 5, Appli
39	38	44.2	108	4	US-09-250-059-5	Sequence 5, Appli
40	38	44.2	108	4	US-09-248-074-5	Sequence 5, Appli
41	38	44.2	108	4	US-09-357-717-5	Sequence 5, Appli
42	38	44.2	108	4	US-09-458-870-5	Sequence 38, Appli
43	38	44.2	108	4	US-09-351-048A-38	Sequence 5, Appli
44	38	44.2	108	4	US-09-248-015-5	Sequence 5, Appli
45	38	44.2	108	4	US-09-544-782-5	Sequence 5, Appli

## ALIGNMENTS

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RESULT 1
US-09-553-498-4
; Sequence 4, Application US/09553498
; Patent No. 6309861
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwartz, Elisabeth
; TITLE OF INVENTION: Process for the production of naturally folded and secreted prote:
; FILE REFERENCE: Case 20379
; CURRENT APPLICATION NUMBER: US/09/553,498
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: EP99107412.1
; PRIOR FILING DATE: 1999-04-26
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 131
; TYPE: PRT
; ORGANISM: E. coli
US-09-553-498-4

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Best Local Similarity 100.0%; Pred. NO. 7.8e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 OKRAAYDQGHAAFEQ 16
Db      84 OKRAAYDQGHAAFEQ 99

RESULT 2
US-09-618-869-4
; Sequence 4, Application US/09618869
; Patent No. 6455279
; GENERAL INFORMATION:
; APPLICANT: Ambrosius, Dorothee
; APPLICANT: Rudolph, Rainer
; APPLICANT: Schaeffner, Joerg
; APPLICANT: Schwartz, Elisabeth
; TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND
; TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
; FILE REFERENCE: 20381
; CURRENT APPLICATION NUMBER: US/09/618,869
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: EP99114811.5
; PRIOR FILING DATE: 1999-07-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 4  
LENGTH: 131  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-09-618-869-4

Query Match 100.0%; Score 86; DB 4; Length 131;  
Best Local Similarity 100.0%; Pred. No. 7.8e-09;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16  
DB 84 QKRAAYDQYGHAAFEQ 99

RESULT 3  
US-09-543-681A-5912  
Sequence 5912, Application US/09543681A  
Patent No. 6605709  
GENERAL INFORMATION:  
APPLICANT: GARY BRETON  
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
FILE REFERENCE: 2709.1002-001  
CURRENT APPLICATION NUMBER: US/09/543.681A  
PRIOR FILING DATE: 2000-04-05  
PRIOR APPLICATION NUMBER: US 60/128.706  
NUMBER OF SEQ ID NOS: 8344  
SEQ ID NO 5912  
LENGTH: 380  
TYPE: PRT  
ORGANISM: Proteus mirabilis  
US-09-543-681A-5912

Query Match 100.0%; Score 86; DB 4; Length 380;  
Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 63 QKRAAYDQYGHAAFEQ 78

RESULT 4  
US-09-489-039A-9011  
Sequence 9011, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709.2004001  
CURRENT APPLICATION NUMBER: US/09/489.039A  
PRIOR FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117.747  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 9011  
LENGTH: 380  
TYPE: PRT  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-9011

Query Match 100.0%; Score 86; DB 4; Length 380;  
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Best Local Similarity 100.0%; Pred. No. 2.4e-07;  
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US-09-553-498-2  
Sequence 2, Application US/09553498  
Patent No. 6309861  
GENERAL INFORMATION:  
APPLICANT: Ambrosius, Dorothee  
APPLICANT: Rudolph, Rainer  
APPLICANT: Schaeffner, Joerg  
APPLICANT: Schwarz, Elisabeth  
TITLE OF INVENTION: Process for the production of naturally folded and secreted protei  
FILE REFERENCE: Case 20379  
CURRENT APPLICATION NUMBER: US/09/553.498  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: EP99107412.1  
NUMBER OF SEQ ID NOS: 10  
SEQ ID NO 2  
LENGTH: 399  
TYPE: PRT  
ORGANISM: E. coli  
US-09-553-498-2

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Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
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QY 1 QKRAAYDQYGHAAFEQ 16  
DB 84 QKRAAYDQYGHAAFEQ 99

RESULT 6  
US-09-618-869-2  
Sequence 2, Application US/09618869  
Patent No. 6455279  
GENERAL INFORMATION:  
APPLICANT: Ambrosius, Dorothee  
APPLICANT: Rudolph, Rainer  
APPLICANT: Schaeffner, Joerg  
APPLICANT: Schwarz, Elisabeth  
TITLE OF INVENTION: PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED AND  
TITLE OF INVENTION: SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR  
FILE REFERENCE: 20381  
CURRENT APPLICATION NUMBER: US/09/618.869  
PRIOR FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: EP9911481.5  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 399  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-09-618-869-2

Query Match 100.0%; Score 86; DB 4; Length 399;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16  
DB 84 QKRAAYDQYGHAAFEQ 99

RESULT 7  
US-08-618-464-4  
Sequence 4, Application US/08618464  
Patent No. 5773570  
GENERAL INFORMATION:  
APPLICANT: CARSON, DENNIS A.  
APPLICANT: ALBANI, SALVATORE  
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN

Query Match 100.0%; Score 86; DB 4; Length 399;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDQYGHAAFEQ 16  
DB 84 QKRAAYDQYGHAAFEQ 99

Query Match 100.0%; Score 86; DB 4; Length 399;  
Best Local Similarity 100.0%; Pred. No. 2.5e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:25:58 ; Search time 11 Seconds  
(without alignments)  
75.738 Million cell updates/sec

Title: US-10-001-938-3

Sequence: 1 QK3AAYDQYGHAFEQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	375	1	DNAJ_ECOLI
2	86	100.0	377	1	DNAJ_HARDU
3	86	100.0	378	1	DNAJ_SALTU
4	86	100.0	382	1	DNAJ_HAETN
5	83	96.5	375	1	DNAJ_ACTAC
6	83	96.5	381	1	DNAJ_VIBCH
7	83	96.5	385	1	DNAJ_VIBHA
8	82	95.3	392	1	NOLC_RHIFR
9	80	93.0	372	1	DNAJ_PASNU
10	77	89.5	234	1	DNAJ_RHILE
11	77	89.5	379	1	DNAJ_RHOSP
12	75	87.2	377	1	DNAJ_BUCOI
13	75	87.2	379	1	DNAJ_PASPA
14	75	87.2	383	1	DNAJ_BUCBP
15	74	86.0	378	1	DNAJ_BUCAP
16	73	84.9	370	1	DNAJ_ERYEH
17	73	84.9	373	1	DNAJ_NEIMA
18	73	84.9	375	1	DNAJ_BROUV
19	73	84.9	377	1	DNAJ_AGRYS
20	73	84.9	377	1	DNAJ_BRAJA
21	73	84.9	377	1	DNAJ_BRUME
22	73	84.9	377	1	DNAJ_BRUSU
23	69	80.2	384	1	DNAJ_RHOCA
24	67	77.9	371	1	DNAJ_METRS
25	66	76.7	383	1	DNAJ_LACSK
26	64	74.4	370	1	DNAJ_RICPR
27	64	74.4	374	1	DNAJ_COXBU
28	63	73.3	376	1	DNAJ_AOUAE
29	63	73.3	379	1	DNAJ_LEGNE
30	62	72.1	377	1	DNAJ_PSEAE
31	58	67.4	379	1	DNAJ_LACIA
32	58	67.4	385	1	DNAJ_CAUCR
33	57	66.3	364	1	DNAJ_BORBU

## ALIGNMENTS

34	57	66.3	369	1	DNAJ_NITEU	O06431 nitrosomona
35	57	66.3	376	1	DNAJ_LISTN	O92bng listeria in
36	57	66.3	377	1	DNAJ_LISMO	O955a3 listeria mo
37	56	65.1	368	1	DNAJ_XYLPA	O9pb06 xyliella fas
38	56	65.1	368	1	DNAJ_XYLFT	O87bs9 xyliella fas
39	56	65.1	378	1	DNAJ_STPRN	P95830 streptococc
40	54	62.8	383	1	DNAJ_PORGI	O9xcae porphyromon
41	53	61.6	307	1	DNAJ_DEIPR	O34136 deinnococcus
42	53	61.6	371	1	DNAJ_ERATY	P48207 francisella
43	52	60.5	372	1	DNAJ_BACSU	P17631 bacillus su
44	52	60.5	376	1	DNAJ_METTH	O27352 methanobact
45	52	60.5	384	1	DNAJ_HALME	O9nhb8 halobacteri

RESULT 1  
DNAJ\_ECOLI  
ID DNAJ\_ECOLI STANDARD; PRT; 375 AA.  
AC P08622;  
DT 01-APR-1998 (Rel. 08, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Chapterone protein dnaJ (Heat shock protein J) (HSP40).  
GN DNAJ OR GRP OR B0015.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-5.  
RX MEDLINE=86111849; PubMed=3003084;  
RA Ohtsuki M., Tamura F., Nishimura S., Uchida H.;  
RT "Nucleotide sequence of the Escherichia coli dnaJ gene and  
RT purification of the gene product";  
RL J. Biol. Chem. 261:1778-1781 (1986).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=86111850; PubMed=3003085;  
RA Bardwell J.C.A., Tilly K., Craig E., King J., Zyllicz M.,  
RA Georgopoulos C.;  
RT "The nucleotide sequence of the Escherichia coli K12 dnaJ gene. A  
RT gene that encodes a heat shock protein.";  
RL J. Biol. Chem. 261:1782-1785 (1986).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=92334977; PubMed=1630901;  
RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,  
RA Isono K., Mizouchi K., Nakata A.;  
RT "Systematic sequencing of the Escherichia coli genome: analysis of  
RT the 0-2.4 min region.";  
RL Nucleic Acids Res. 20:3305-3308 (1992).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shaoy Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1234-1238 (1997).  
RN [5]  
RP POSSIBLE FUNCTION.  
RX MEDLINE=91187894; PubMed=1826368;  
RA Liberek K., Marszalek J., Ang D., Georgopoulos C., Zyllicz M.;  
RT "Escherichia coli DnaJ and GrpE heat shock proteins jointly stimulate  
RT ATPase activity of DnaK.";  
RL Proc. Natl. Acad. Sci. U.S.A. 88:2874-2878 (1991).  
RN [6]

RP STRUCTURE BY NMR OF 1-107.  
 RX MEDLINE=96291434; PubMed=8764403;  
 RA Pellechia M., Szyperski T., Wall D., Georgopoulos C., Wuehrich K.;  
 RT "NMR structure of the J-domain and the Gly/Phe-rich region of the  
 RL Escherichia coli DnaJ chaperone.";  
 RN J. Mol. Biol. 260:236-250(1996).  
 [7]  
 RP STRUCTURE BY NMR OF 1-104.  
 RX MEDLINE=99224904; PubMed=10210198;  
 RA Huang K., Flanagan J.M., Prestegard J.H.;  
 RT "The influence of C-terminal extension on the structure of the 'J'-  
 RL domain' in E. coli DnaJ.";  
 RN Protein Sci. 8:203-214(1999).  
 [8]  
 RP STRUCTURE BY NMR OF 130-208.  
 RX MEDLINE=20351465; PubMed=10891270;  
 RA Martinez-Yamout M., Legge G.B., Zhang O., Wright P.E., Dyson H.J.;  
 RT "Solution structure of the cysteine-rich domain of the Escherichia  
 RL coli chaperone protein DnaJ.";  
 RN J. Mol. Biol. 300:805-818(2000).  
 CC -1- FUNCTION: INTERACTS WITH DNAK TO DISASSEMBLE A PROTEIN COMPLEX  
 AT THE PHAGE LAMBDA ORIGIN OF REPLICATION. STIMULATES, JOINTLY  
 WITH GRPE, THE ATPASE ACTIVITY OF DNAK.  
 CC -1- COFACTOR: Binds 2 zinc ions per monomer.  
 CC -1- SUBUNIT: Homodimer.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- INDUCTION: BY HEAT SHOCK UNDER THE CONTROL OF THE HTRP REGULATORY  
 PROTEIN.  
 CC -1- SIMILARITY: Belongs to the dnaJ family.  
 CC -1- SIMILARITY: Contains 1 J domain.  
 CC -1- SIMILARITY: Contains 1 CR domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; M12565; AAA23693.1; -;  
 DR EMBL; D10483; BAB96590.1; -;  
 DR EMBL; A8000112; AAC73126.1; -;  
 DR PIR; A92572; HHECDJ.  
 DR PDB; 1XBL; 11-JUN-97.  
 DR PDB; 1BQJ; 15-JUN-99.  
 DR PDB; 1EXX; 25-JUL-00.  
 DR ECODBASE; H036.5; 6TH EDITION.  
 DR Ecogene; EG10240; dnaJ.  
 DR InterPro; IPR002939; DnaJ\_C.  
 DR InterPro; IPR001305; DnaJ\_CXXCXG.  
 DR InterPro; IPR001623; DnaJ\_N.  
 DR InterPro; IPR008971; HSP40\_DnaJ\_p.  
 DR InterPro; IPR003095; Hsp\_DnaJ.  
 DR Pfam; PF00226; DnaJ; 1.  
 DR Pfam; PF01556; DnaJ\_C; 1.  
 DR Pfam; PF00684; DnaJ\_CXXCXG; 1.  
 DR PRINTS; PRO0625; DNADPROTEIN.  
 DR SMART; SM00271; DnaJ; 1.  
 DR PROSITE; PS00636; DnaJ\_1; 1.  
 DR PROSITE; PS0076; DnaJ\_2; 1.  
 DR PROSITE; PS00637; DnaJ\_CXXCXG; 1.  
 KM Chaperone; DNA replication; Heat shock; Repeat; Zinc; Metal-binding;  
 KM 3D-structure; Complete proteome.  
 FT INIT MET 0  
 FT DOMAIN 71 J-DOMAIN.  
 FT 76 113 GLY-RICH.  
 FT REPEAT 143 150 CXXCXGXG MOTIF.  
 FT REPEAT 160 167 CXXCXGXG MOTIF.  
 FT REPEAT 182 189 CXXCXGXG MOTIF.  
 FT REPEAT 196 203 CXXCXGXG MOTIF.  
 FT METAL 143 143 ZINC 1.

FT METAL 146 146 ZINC 1.  
 FT METAL 160 160 ZINC 2.  
 FT METAL 163 163 ZINC 2.  
 FT METAL 182 182 ZINC 2.  
 FT METAL 185 185 ZINC 2.  
 FT METAL 196 196 ZINC 1.  
 FT METAL 199 199 ZINC 1.  
 FT HELIX 5 8  
 FT TURN 9 10  
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 FT HELIX 18 31  
 FT TURN 32 35  
 FT HELIX 36 38  
 FT TURN 41 42  
 FT HELIX 43 50  
 FT TURN 51 51  
 FT HELIX 52 56  
 FT HELIX 59 64  
 FT HELIX 65 67  
 FT TURN 68 73  
 FT TURN 131 133  
 FT TURN 140 142  
 FT STRAND 144 146  
 FT HELIX 147 149  
 FT TURN 151 151  
 FT STRAND 158 159  
 FT TURN 161 165  
 FT STRAND 168 173  
 FT TURN 174 175  
 FT STRAND 176 181  
 FT TURN 183 187  
 FT STRAND 190 191  
 FT STRAND 195 195  
 FT HELIX 197 199  
 FT TURN 200 201  
 FT STRAND 204 206  
 SQ SEQUENCE 375 AA; 40969 MW; 8DE1863CC0BD8C3F CRC64;  
 Query Match 100.0%; Score 86; DB 1; Length 375;  
 Best Local Similarity 100.0%; Pred. No. 2e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 QKRAVYDYGHAAPFQ 16  
 DB 60 QKRAVYDYGHAAPFQ 75  
 RESULT 2  
 ID DNAD HAEDU STANDARD; PRT; 377 AA.  
 AC P48208;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Chaperone protein dnaJ.  
 GN DNAD OR HD0188.  
 OS Haemophilus ducreyi.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus.  
 OC NCBI\_TaxID=730;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=35000HP / ATCC 700724;  
 RA Parsons L.M.;  
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=35000HP / ATCC 700724;  
 RA Munson R.S., Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,  
 RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;  
 RT "The complete genome sequence of Haemophilus ducreyi";  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Acts as a co-chaperone. Stimulates, jointly with grpe,

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:29:38 ; Search time 20 Seconds

(without alignments)  
76.953 Million cell updates/sec

Title: US-10-001-938-3

Perfect score: 86

Sequence: 1 OKRAAYDQGHAFEEQ 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:  
2: p1r2:  
3: p1r3:  
4: p1r4:

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	376	1	HRECDU
2	86	100.0	376	2	G90630
3	86	100.0	376	2	G85481
4	86	100.0	379	2	AB0058
5	86	100.0	379	2	AF0503
6	86	100.0	394	2	C64112
7	83	96.5	381	2	D82270
8	82	95.3	392	2	S15295
9	82	97.2	377	2	UC8609
10	75	87.2	377	2	F84947
11	73	84.9	373	2	B47042
12	73	84.9	373	2	AC3502
13	73	84.9	377	2	AD5591
14	73	84.9	377	2	D93737
15	74	84.9	357	2	I40843
16	74	84.9	370	2	C71729
17	63	74.4	376	2	B70361
18	63	72.1	190	2	B53588
19	62	72.1	377	2	A83052
20	62	72.1	373	2	H97728
21	58	67.4	379	2	A47079
22	58	67.4	379	2	H86902
23	58	67.4	385	2	C87250
24	58	67.4	385	2	A48210
25	57	66.3	364	2	D70164
26	57	66.3	376	2	AD1621
27	57	66.3	377	2	T43739
28	57	66.3	377	2	AH1258
29	57	66.3	377	2	AH1258

30	56	65.1	368	2	F82570	DnaJ protein XP233
31	56	65.1	372	2	H97928	heat-shock protein
32	56	65.1	378	2	D95060	dnaJ protein [lipo
33	53	61.6	499	2	G96831	hypothetical prote
34	52	60.5	372	2	B41874	heat shock protein
35	52	60.5	376	2	H69038	heat shock protein
36	52	60.5	389	2	S41748	heat shock protein
37	50	58.1	297	2	G81329	heat shock protein
38	50	58.1	348	2	T04618	probable curved-DN
39	50	58.1	379	2	B89939	DnaJ protein [lipo
40	50	58.1	383	2	E90603	heat shock protein
41	50	58.1	416	2	F71379	heat shock protein
42	49	57.0	335	2	T48161	heat shock protein
43	49	57.0	346	2	B84602	probable DnaJ prot
44	49	57.0	370	2	D38181	heat-shock protein
45	49	57.0	375	2	D82894	heat shock protein

## ALIGNMENTS

RESULT 1  
HRECDU  
heat shock protein dnaJ - Escherichia coli (strain K-12)  
C:Species: Escherichia coli  
C:Date: 30-Jun-1988 #sequence revision 30-Jun-1988 #text\_change 01-Mar-2002  
C:Accession: A92572; A26298; S40537; G64721; A26299  
R:Barwell, J.C.A.; Tilly, K.; Craig, E.; King, J.; Zylitz, M.; Georgopoulos, C.  
U. Biol. Chem. 261, 1782-1785, 1986  
A:Title: The nucleotide sequence of the Escherichia coli K12 dnaJ gene.  
A:Reference number: A92572; MUID:86111850; PMID:3003085  
A:Accession: A92572  
A:Molecule type: DNA  
A:Residues: 1-376 <BAR>  
A:Cross-references: GB:M2565; NID:g145767; PIDN:AAA23693.1; PID:g145769  
A:Experimental source: strain K12  
R:Ohki, M.; Tamura, F.; Nishimura, S.; Uchida, H.  
U. Biol. Chem. 261, 1778-1781, 1986  
A:Title: The complete genome sequence of Escherichia coli dnaJ gene and purification of the g  
A:Reference number: A26298; MUID:86111849; PMID:3003084  
A:Accession: A26298  
A:Molecule type: DNA  
A:Residues: 1-376 <OHK>  
A:Cross-references: GB:D10483; GB:J01597; GB:J01683; GB:J01706; GB:K01298; GB:K01390; GB:K01391; GB:K01392; GB:K01393; GB:K01394; GB:K01395; GB:K01396; GB:K01397; GB:K01398; GB:K01399; GB:K01400; GB:K01401; GB:K01402; GB:K01403; GB:K01404; GB:K01405; GB:K01406; GB:K01407; GB:K01408; GB:K01409; GB:K01410; GB:K01411; GB:K01412; GB:K01413; GB:K01414; GB:K01415; GB:K01416; GB:K01417; GB:K01418; GB:K01419; GB:K01420; GB:K01421; GB:K01422; GB:K01423; GB:K01424; GB:K01425; GB:K01426; GB:K01427; GB:K01428; GB:K01429; GB:K01430; GB:K01431; GB:K01432; GB:K01433; GB:K01434; GB:K01435; GB:K01436; GB:K01437; GB:K01438; GB:K01439; GB:K01440; GB:K01441; GB:K01442; GB:K01443; GB:K01444; GB:K01445; GB:K01446; GB:K01447; GB:K01448; GB:K01449; GB:K01450; GB:K01451; GB:K01452; GB:K01453; GB:K01454; GB:K01455; GB:K01456; GB:K01457; GB:K01458; GB:K01459; GB:K01460; GB:K01461; GB:K01462; GB:K01463; GB:K01464; GB:K01465; GB:K01466; GB:K01467; GB:K01468; GB:K01469; GB:K01470; GB:K01471; GB:K01472; GB:K01473; GB:K01474; 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F,183-190/Region: CXXCXGXG repeat  
F,197-204/Region: CXXCXGXG repeat

Query Match 100.0%; Score 86; DB 1; Length 376;  
Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFEQ 16  
|||||  
61 OKRAAYDQYGHAAFEQ 76

## RESULT 2

G90630  
DnaJ protein [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0506952)  
C/Species: Escherichia coli  
C/Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
C/Accession: G90630

R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;  
Gasanara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gend  
A/Reference number: A59629; MUID:21156231; PMID:11558796  
A/Accession: G90630

A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-376 <HAY>  
A/Cross-references: GB:BA000007; PIDN:BA833438.1; PID:G13359471; GSPDB:GN00154  
A/Experimental source: strain O157:H7, substrain RIMD 0509952  
C/Genetics:

A/Gene: EC60015  
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 376;  
Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFEQ 16  
|||||  
61 OKRAAYDQYGHAAFEQ 76

## RESULT 3

G85481  
Chaperone with DnaK, heat shock protein [imported] - Escherichia coli (strain O157:H7, S  
C/Species: Escherichia coli  
C/Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C/Accession: G85481

R.Gerna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
Hiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
Nature 409, 529-533, 2001  
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A/Reference number: A85480; MUID:21074935; PMID:11206551  
A/Accession: G85481

A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-376 <STO>  
A/Cross-references: GB:AE005174; NID:G12512693; PIDN:AAC54315.1; GSPDB:GN00145; UMGF:Z00  
A/Experimental source: strain O157:H7, substrain EDL933  
C/Genetics:

A/Gene: dnaJ  
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 376;  
Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFEQ 16  
|||||  
61 OKRAAYDQYGHAAFEQ 76

## RESULT 4

AB0058  
Chaperone protein DnaJ [imported] - Yersinia pestis (strain C092)

C/Species: Yersinia pestis  
C/Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 03-Nov-2001  
C/Accession: AB0058  
R.Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.;  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, I

Nature 413, 523-527, 2001  
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A/Reference number: AB0001; MUID:21470413; PMID:11586360  
A/Accession: AB0058

A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-379 <KUR>  
A/Cross-references: GB:AL590842; PIDN:CAC89325.1; PID:G15978561; GSPDB:GN00175  
C/Genetics:

A/Gene: dnaJ  
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 379;  
Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFEQ 16  
|||||  
61 OKRAAYDQYGHAAFEQ 76

## RESULT 5

AF0503  
DnaJ protein [imported] - Salmonella enterica subsp. enterica serovar Typh (strain CT18)

C/Species: Salmonella enterica subsp. enterica serovar Typh  
A/Note: This species has also been called Salmonella typhi  
C/Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 18-Nov-2002  
C/Accession: AF0503  
R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,  
th, T.; Comercon, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Garra, P.

Nature 413, 848-852, 2001  
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A/Reference number: AB0502; MUID:21534947; PMID:11677608  
A/Accession: AF0503

A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-379 <PAR>  
A/Cross-references: GB:AU513382; PIDN:CAD01166.1; PID:G16501296; GSPDB:GN00176  
C/Genetics:

A/Gene: STY0013  
C/Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Query Match 100.0%; Score 86; DB 2; Length 379;  
Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDQYGHAAFEQ 16  
|||||  
61 OKRAAYDQYGHAAFEQ 76

## RESULT 6

C64112  
heat shock protein dnaJ - Haemophilus influenzae (strain Rd KW20)

C/Species: Haemophilus influenzae  
C/Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 20-Aug-1999  
C/Accession: C64112  
R.Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kestlavage, A.  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.  
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Georgagen, N.S.M.  
Science 269, 496-512, 1995  
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.

A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.





CC immunological disorder (e.g. autoimmune disease such as arthritis or  
 CC articular juvenile idiopathic arthritis), an infectious disease, an  
 CC inflammatory bowel disease or cancer. The immunogenic peptide of the  
 CC invention is also useful for modulating immunoeffector cell  
 CC responsiveness in a subject. The immunogenic peptide is particularly  
 CC useful for treating the above-mentioned diseases in mammals, e.g. cat,  
 CC dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In  
 CC general, the peptide is useful in methods involving mucosal tolerisation,  
 CC DNA vaccination, allergy induction or active immunisation. The present  
 CC sequence represents an *E. coli* DNA immunogenic peptide of the invention  
 CC  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 86; DB 5; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFEQ 16  
 |||||  
 Db 1 OKRAAYDQYGHAAFEQ 16

## RESULT 2

ABR55126  
 ID ABR55126 standard; peptide; 16 AA.

AC ABR55126;

DT 03-JUL-2003 (first entry)

E. coli dnaB1 antigen-specific epitope peptide.

Antigen-specific epitope; immune response; T cell; cytokine;  
 antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;  
 cytosarctic; antithyroid; antiasthmatic; immunosuppressive;  
 antipsoriatic; anti-ulcer; antianaemic; cardiant; respiratory;  
 antiallergic; dermatological; antipsoriatic.

XX Escherichia coli.

OS W02003026579-A2.

PN 03-APR-2003.

PF 25-SEP-2002; 2002WC-US030578.

PR 25-SEP-2001; 2001US-0325499P.

PR 11-DEC-2001; 2001US-0339284P.

PA (REGC) UNIV CALIFORNIA.

PI Albani S, Martins A;

DR WPI; 2003-430097/40.

Modulating an immune response in a subject having an immune-related  
 disorder, e.g. arthritis by administering an antigen-specific epitope and  
 a cytokine or an agent that effects cytokine activity or expression.  
 Disclosure; Page 9; 41pp; English.

CC The invention relates to a novel method for modulating an immune response  
 CC in a subject having an immune-related disorder. The method comprises: (a)  
 CC administering an antigen-specific epitope, where administration provides  
 CC epitope-specific T cell immune modulation; and (b) administering a  
 CC cytokine, an agent that effects cytokine activity or expression, or an  
 CC antidiabetic therapy. The method of the invention has antarthritic,  
 CC antidiabetic, neuroprotective, anti-inflammatory, cytosarctic,  
 CC antithyroid, anti-asthmatic, immunosuppressive, antipsoriatic, anti-  
 CC ulcer, antianaemic, cardiant, respiratory general, antiallergic, anti-  
 CC dermatological, and antipsoriatic activity. The method is useful for  
 CC modulating an immune response in a subject having an immune-related  
 CC disorder. The present sequence is used in the exemplification of the

CC invention  
 XX  
 SQ Sequence 16 AA;

Query Match 100.0%; Score 86; DB 6; Length 16;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-08;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFEQ 16  
 |||||  
 Db 1 OKRAAYDQYGHAAFEQ 16

## RESULT 3

AA11396  
 ID AA11396 standard; protein; 131 AA.

AC AA11396;

DT 22-FEB-2001 (first entry)

E. coli expression plasmid pUB5520-pIN-5-Domain encoded protein.

Eukaryotic protein; protease; interferon; antibody; hormone;  
 disulfide bridge.

XX Escherichia coli.

OS Synthetic.

PN EP1048732-A1.

PD 02-NOV-2000.

PF 26-APR-1999; 99EP-00107412.

PR 26-APR-1999; 99EP-00107412.

PA (HOPE) HOFFMANN LA ROCHE & CO AG F.

DR WPI: 2000-674185/66.

DR N-PSDB; AAC66072.

Preparation of water-soluble eukaryotic polypeptides with disulfide  
 bridges e.g. rPA, comprises cultivation of prokaryotic cells in the  
 presence of arginine or amide compound.

Example 3; Page 17; 40pp; German.

CC This invention describes a novel preparation of a water-soluble,  
 CC naturally occurring eukaryotic polypeptide containing two or more  
 CC cysteine units bound via a disulfide bridge which comprises cultivation  
 CC of prokaryotic cells in the presence of arginine or an amide compound.  
 CC The method is useful for the preparation of eukaryotic proteins e.g.  
 CC proteases, interferons, protein hormones, antibodies or antibody  
 CC fragments (e.g. a single chain Fv fragment that binds to thyroid  
 CC stimulating hormone). It is especially useful for preparing proteins with  
 CC more than five disulfide bridges, e.g. recombinant plasminogen activator  
 CC (rPA). The technique is simple and does not require in vitro after-  
 CC treatment, such as the removal of inclusion bodies, reduction or  
 CC naturalization

SQ Sequence 131 AA;

Query Match 100.0%; Score 86; DB 3; Length 131;  
 Best Local Similarity 100.0%; Pred. No. 4e-07;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 OKRAAYDQYGHAAFEQ 16  
 |||||  
 Db 84 OKRAAYDQYGHAAFEQ 99

## RESULT 4

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 11, 2004, 09:41:15 ; Search time 44 Seconds  
(without alignments)  
113.425 Million cell updates/sec

Title: US-10-001-938-3  
Perfect score: 86  
Sequence: 1 OKRAAYDQYGHAFEQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues  
Total number of hits satisfying chosen parameters: 218390

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	100.0	16	US-10-001-938-3	Sequence 3, Appl1
2	81	94.2	15	US-09-756-983-10	Sequence 10, Appl1
3	81	94.2	15	US-09-828-574-10	Sequence 27, Appl1
4	81	94.2	15	US-10-001-938-27	Sequence 4, Appl1
5	81	94.2	15	US-10-299-540-4	Sequence 4, Appl1
6	81	94.2	15	US-10-299-184-4	Sequence 444, App
7	81	94.2	15	US-10-239-313A-444	Sequence 447, App
8	81	94.2	15	US-10-239-313A-447	Sequence 11, Appl1
9	72	83.7	15	US-09-828-574-11	Sequence 5, Appl1
10	72	83.7	15	US-10-299-540-5	Sequence 5, Appl1
11	72	83.7	15	US-10-299-184-5	Sequence 6, Appl1
12	54	62.8	15	US-10-299-540-6	Sequence 6, Appl1
13	54	62.8	15	US-10-299-184-6	Sequence 154, App
14	34	39.5	9	US-10-283-423-154	Sequence 155, App
15	34	39.5	9	US-10-283-423-155	

16	34	39.5	9	US-10-283-423-157	Sequence 157, App
17	34	39.5	9	US-10-283-423-158	Sequence 158, App
18	34	39.5	9	US-10-283-423-159	Sequence 159, App
19	34	39.5	9	US-10-213-821-154	Sequence 154, App
20	34	39.5	9	US-10-213-821-155	Sequence 155, App
21	34	39.5	9	US-10-213-821-157	Sequence 157, App
22	34	39.5	9	US-10-213-821-158	Sequence 158, App
23	34	39.5	9	US-10-213-821-159	Sequence 159, App
24	34	39.5	9	US-10-736-048-154	Sequence 154, App
25	34	39.5	9	US-10-736-048-155	Sequence 155, App
26	34	39.5	9	US-10-736-048-157	Sequence 157, App
27	34	39.5	9	US-10-736-048-158	Sequence 158, App
28	34	39.5	9	US-10-736-048-159	Sequence 159, App
29	34	39.5	14	US-10-161-959-6	Sequence 6, Appl1
30	34	39.5	14	US-10-283-423-160	Sequence 160, App
31	34	39.5	14	US-10-213-821-160	Sequence 160, App
32	34	39.5	14	US-10-736-048-160	Sequence 160, App
33	34	39.5	15	US-09-756-983-11	Sequence 11, Appl1
34	34	39.5	15	US-10-161-959-5	Sequence 5, Appl1
35	34	39.5	15	US-10-299-540-7	Sequence 7, Appl1
36	34	39.5	15	US-10-299-540-8	Sequence 8, Appl1
37	34	39.5	15	US-10-299-184-7	Sequence 7, Appl1
38	34	39.5	15	US-10-299-184-8	Sequence 8, Appl1
39	34	39.5	15	US-10-239-313A-443	Sequence 443, App
40	32	37.2	13	US-10-088-887-58	Sequence 58, Appl1
41	31	36.0	14	US-10-161-959-28	Sequence 28, Appl1
42	31	36.0	15	US-09-841-091B-10	Sequence 10, Appl1
43	31	36.0	15	US-10-056-563-10	Sequence 30, Appl1
44	31	36.0	15	US-10-161-959-10	Sequence 10, Appl1
45	31	36.0	15	US-10-251-703-10	Sequence 10, Appl1

ALIGNMENTS

RESULT 1  
US-10-001-938-3  
Publication No. US20030031679A1  
GENERAL INFORMATION:  
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA  
APPLICANT: ALBANI, Salvatore  
APPLICANT: CARSON, Dennis  
APPLICANT: PRAKSEN, Berent  
APPLICANT: MARTINI, Alberto  
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND US1  
FILE REFERENCE: US01360-1  
CURRENT APPLICATION NUMBER: US/10/001,938  
CURRENT FILING DATE: 2001-10-31  
PRIOR APPLICATION NUMBER: US 60/245,181  
PRIOR FILING DATE: 2000-11-01  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 3  
LENGTH: 16  
TYPE: PRT  
ORGANISM: Escherichia coli  
US-10-001-938-3  
Query Match 100.0%; Score 86; DB 14; Length 16;  
Best Local Similarity 100.0%; Pred. No. 9.3e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 OKRAAYDQYGHAFEQ 16  
Db 1 OKRAAYDQYGHAFEQ 16  
RESULT 2  
US-09-756-983-10  
Sequence 10, Application US/09756983  
Patent No. US20020122818A1

```

; GENERAL INFORMATION:
; APPLICANT: Albani, Salvatore
; TITLE OF INVENTION: METHODS FOR ISOLATION, QUANTIFICATION,
; TITLE OF INVENTION: CHARACTERIZATION AND MODULATION OF
; TITLE OF INVENTION: ANTIGEN-SPECIFIC T CELLS
; FILE REFERENCE: 246/285-CIP
; CURRENT APPLICATION NUMBER: US/09/756,983
; CURRENT FILING DATE: 2001-01-09
; PRIOR APPLICATION NUMBER: 60/105,018
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: 09/421,506
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: PCT/US99/2466
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli
; FEATURE:
; OTHER INFORMATION: dnaUp1 heat shock protein
; US-09-756-983-10

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Query Match          94.2%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6,1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 OKRAAYDQYGHAAFE 15
Db      1 OKRAAYDQYGHAAFE 15

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RESULT 3
US-09-828-574-10
; Sequence 10, Application US/09828574
; Patent No. US20020146759A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore
; APPLICANT: PRAKKEN, Berent J.
; TITLE OF INVENTION: STRESS PROTEINS AND PEPTIDES AND METHODS OF USE THEREOF
; FILE REFERENCE: UCSD1310-1
; CURRENT APPLICATION NUMBER: US/09/828,574
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/224,104
; PRIOR FILING DATE: 2000-08-09
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: dnaUp1 peptide
; US-09-828-574-10

```

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Query Match          94.2%; Score 81; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6,1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 OKRAAYDQYGHAAFE 15
Db      1 OKRAAYDQYGHAAFE 15

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RESULT 4
US-10-001-938-27
; Sequence 27, Application US/10001938
; Publication No. US20030031679A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: ALBANI, Salvatore

```

```

; APPLICANT: CARSON, Dennis
; APPLICANT: PRAKKEN, Berent
; APPLICANT: MARTINI, Alberto
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES DERIVED FROM HEAT SHOCK PROTEINS AND USE
; TITLE OF INVENTION: THEROF
; FILE REFERENCE: UCSD1360-1
; CURRENT APPLICATION NUMBER: US/10/001,938
; CURRENT FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: US 60/245,181
; PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-10-001-938-27

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```

Query Match          94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6,1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 OKRAAYDQYGHAAFE 15
Db      1 OKRAAYDQYGHAAFE 15

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```

RESULT 5
US-10-299-540-4
; Sequence 4, Application US/10299540
; Publication No. US2003014338A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: CARSON, Dennis A.
; APPLICANT: ALBANI, Salvatore
; TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN INDUCING IMMUNE PROTECT
; TITLE OF INVENTION: AGAINST ARTHRITIS
; FILE REFERENCE: UCSD1370-7
; CURRENT APPLICATION NUMBER: US/10/299,540
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: US 09/616,247
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/107,615
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 08/618,464
; PRIOR FILING DATE: 1996-03-15
; PRIOR APPLICATION NUMBER: US 08/246,988
; PRIOR FILING DATE: 1994-05-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic dnaUp1
; US-10-299-540-4

```

```

Query Match          94.2%; Score 81; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 6,1e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      1 OKRAAYDQYGHAAFE 15
Db      1 OKRAAYDQYGHAAFE 15

```

```

RESULT 6
US-10-299-184-4
; Sequence 4, Application US/10299184
; Publication No. US20030147910A1
; GENERAL INFORMATION:

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 11, 2004, 09:38:55 ; Search time 20 Seconds

(without alignments)  
76,953 Million cell updates/sec

Title: US-10-001-938-3

Sequence: 1 QKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 2772

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

PIR 78:.\*  
1: p1r1:.\*  
2: p1r2:.\*  
3: p1r3:.\*  
4: p1r4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	39.5	11	2	A60656
2	34	39.5	14	2	A56632
3	31	36.0	10	1	GMROL2
4	31	36.0	10	2	B60656
5	31	36.0	13	2	S47372
6	31	36.0	11	2	S47384
7	30	34.9	11	1	GMROL
8	30	34.9	13	2	S47368
9	30	34.9	13	2	S47359
10	28	32.6	13	2	S47365
11	28	32.6	13	2	S47374
12	26	30.2	11	2	PT0214
13	26	30.2	13	2	S47388
14	26	30.2	13	2	PH1479
15	26	30.2	14	4	I52618
16	26	30.2	15	2	PH0770
17	25	29.1	13	2	S32471
18	25	29.1	14	2	PH1586
19	24	27.9	16	2	PH1622
20	24	27.9	16	2	PH1589
21	23	26.7	8	2	S11078
22	23	26.7	13	2	S32472
23	23	26.7	13	2	A60379
24	23	25.6	13	2	S32473
25	22	25.6	13	2	S47383
26	22	25.6	13	2	PH1319
27	22	25.6	15	2	F28587
28	22	25.6	15	2	I53284
29	21	24.4	10	2	PT0215

30	21	24.4	12	2	PH0746	T-cell receptor be
31	21	24.4	12	2	PH1461	T-cell receptor be
32	21	24.4	12	2	PH0771	T-cell receptor be
33	21	24.4	13	2	S32474	lymadpamide 4 - g
34	21	24.4	13	2	S47361	T-cell antigen rec
35	21	24.4	13	2	I51905	collecting duct wa
36	21	24.4	14	2	S48685	extension protein
37	21	24.4	14	2	G44957	photosystem II oxy
38	21	24.4	14	2	PH0755	T-cell receptor be
39	21	24.4	14	2	A17150	glucose 1-dehydrog
40	21	24.4	15	2	PC4269	unidentified OR310
41	20	23.3	10	2	PT0309	Ig heavy chain CRD
42	20	23.3	13	2	G22565	R-phycocerythrin ga
43	20	23.3	13	2	PH0168	phosphopyruvate hy
44	20	23.3	14	2	PA0013	photosystem II oxy
45	20	23.3	14	2	PT0232	Ig heavy chain CRD

#### ALIGNMENTS

##### RESULT 1

A60656  
perisulfakinin - American cockroach  
C:Species: Periplaneta americana (American cockroach)  
C:Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 11-Jul-1997  
C:Accession: A60656  
R:Venestra, U.A.  
Neuropeptides 14, 145-149, 1989  
A:Title: Isolation and structure of two gastrin/CKK-like neuropeptides from the American  
A:Reference number: A60656; MUID:90137290; PMID:2615921  
A:Accession: A60656  
A:Molecule type: protein  
A:Residues: 1-11 <VBB>  
C:Comment: This neuropeptide stimulates hindgut contractions.  
C:Keywords: amidated carboxyl end; neuropeptide; sulfoprotein  
F:6/Binding site: sulfite (Tyr) (covalent) #status experimental  
F:11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 39.5%; Score 34; DB 2; Length 11;  
Best Local Similarity 55.6%; Pred. No. 9;  
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDQYGHAAAP 14  
Db 3 FDDYGHMRF 11

##### RESULT 2

A56632  
neousulfakinin-II - flesh fly (Sarcophaga bullata)  
N:Alternate names: Neb-SK-II  
N:Contains: neousulfakinin-I (Neb-SK-I)  
C:Species: Sarcophaga bullata  
C:Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 20-Jun-2000  
C:Accession: A56632  
R:Fontagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; De Loof, A.  
Comp. Biochem. Physiol. C 103, 135-142, 1992  
A:Title: Isolation and primary structure of two sulfakinin-like peptides from the flesh fly  
A:Reference number: A56632; MUID:93083101; PMID:1360367  
A:Accession: A56632

A:Molecule type: protein  
A:Residues: 1-14 <FON>  
A:Experimental source: heads  
A>Note: sequence extracted from NCBI backbone (NCBIP:120391)  
C:Keywords: amidated carboxyl end; neuropeptide; sulfoprotein  
F:1-14/Product: neousulfakinin-II #status experimental <NSK2>  
F:6-14/Product: neousulfakinin-I #status experimental <NSK1>  
F:9/Binding site: sulfite (Tyr) (covalent) #status predicted  
F:14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 39.5%; Score 34; DB 2; Length 14;  
Best Local Similarity 55.6%; Pred. No. 12;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDYGHAAP 14  
: |||||  
Db 6 FDYGHMRF 14

## RESULT 3

GNROL2  
leucosulfakinin-II - Madeira cockroach  
N,Alternate names: LSK-II  
C,Species: Leucophaea maderae (Madeira cockroach)  
C,Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 13-Sep-1996  
C,Accession: A26335  
R,Nachman, R.J.; Holman, G.M.; Cook, B.J.; Haddon, W.F.; Ling, N.  
Biochem. Biophys. Res. Commun. 140, 357-364, 1986  
A,Title: Leucosulfakinin-II, a blocked sulfated insect neuropeptide with homology to chc  
A,Reference number: A26335, MUID:87048769; PMID:3778455  
A,Accession: A26335  
A,Molecule type: protein  
A,Residues: 1-10 <NAC>  
C,Comment: This peptide was isolated from head extracts. It stimulates muscle contractile  
C,Superfamily: gastrin  
C,Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; sulfoprotein  
F,5/Binding site: sulfate (Tyr) (covalent) #status experimental  
F,10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 36.0%; Score 31; DB 1; Length 10;  
Best Local Similarity 62.5%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 DQYGHAP 14  
: |||||  
Db 3 DDYGHMRF 10

## RESULT 4

B60656  
leucosulfakinin II, non-sulfated - American cockroach  
C,Species: Periplaneta americana (American cockroach)  
C,Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 08-Dec-1995  
C,Accession: B60656  
R,Veenstra, J.A.  
Neuropeptides 14, 145-149, 1989  
A,Title: Isolation and structure of two gastrin/CCK-like neuropeptides from the American  
A,Reference number: A60656; MUID:90137190; PMID:2615921  
A,Accession: B60656  
A,Molecule type: protein  
A,Residues: 1-10 <VEE>  
C,Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid  
F,1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F,10/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 36.0%; Score 31; DB 2; Length 10;  
Best Local Similarity 62.5%; Pred. No. 27;  
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 DQYGHAP 14  
: |||||  
Db 3 DDYGHMRF 10

## RESULT 5

S47372  
T-cell antigen receptor VJ junction beta chain - human  
C,Species: Homo sapiens (man)  
C,Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C,Accession: S47372  
R,Lehner, P.J.  
submitted to the EMBL Data Library, August 1994  
A,Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T c  
Reference number: S47355

A,Accession: S47372  
A,Status: preliminary  
A,Molecule type: mRNA  
A,Residues: 1-13 <LEH>  
A,Cross-references: EMBL:Z35697; NID:G527485; PIDN:CAA84766.1; PID:G527486  
C,Keywords: T-cell receptor

Query Match 36.0%; Score 31; DB 2; Length 13;  
Best Local Similarity 71.4%; Pred. No. 36;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAYDOY 9  
: |||||  
Db 6 RSYDOY 12

## RESULT 6

S47384  
T-cell antigen receptor VJ junction beta chain - human  
C,Species: Homo sapiens (man)  
C,Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999  
C,Accession: S47384  
R,Lehner, P.J.  
submitted to the EMBL Data Library, August 1994  
A,Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce  
A,Reference number: S47355  
A,Accession: S47384  
A,Status: preliminary  
A,Molecule type: mRNA  
A,Residues: 1-13 <LEH>  
A,Cross-references: EMBL:Z35704; NID:G527501; PIDN:CAA84773.1; PID:G527502  
C,Keywords: T-cell receptor

Query Match 36.0%; Score 31; DB 2; Length 13;  
Best Local Similarity 71.4%; Pred. No. 36;  
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RAYDOY 9  
: |||||  
Db 6 RSYDOY 12

## RESULT 7

GNROL  
leucosulfakinin - Madeira cockroach  
N,Alternate names: LSK  
C,Species: Leucophaea maderae (Madeira cockroach)  
C,Date: 17-Mar-1987 #sequence\_revision 17-Mar-1987 #text\_change 13-Sep-1996  
C,Accession: A01622  
R,Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.  
Science 234, 71-73, 1986  
A,Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and chc  
A,Reference number: A01622; MUID:86315858; PMID:3749893  
A,Accession: A01622  
A,Molecule type: protein  
A,Residues: 1-11 <NAC>  
C,Superfamily: gastrin  
C,Keywords: amidated carboxyl end; hormone; sulfoprotein  
F,6/Binding site: sulfate (Tyr) (covalent) #status experimental  
F,1/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 34.9%; Score 30; DB 1; Length 11;  
Best Local Similarity 44.4%; Pred. No. 45;  
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 YDYGHAAP 14  
: |||||  
Db 3 FDYGHMRF 11

## RESULT 8

S47368  
T-cell antigen receptor VJ junction beta chain - human

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:34:09 ; Search time 11 Seconds

(without alignments)  
75.738 Million cell updates/sec

Title: US-10-001-938-3

Sequence: 1 QXRAAYDQYGHAAFEQ 16

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 880

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	34	39.5	9 1	NSK1_SARBU
2	34	39.5	11 1	LSKP_PERAM
3	34	39.5	14 1	NSK2_SARBU
4	33	38.4	12 1	LSK2_LOCOMI
5	31	36.0	10 1	LSK2_LEUMA
6	30	34.9	11 1	NP1_LEUMA
7	25	29.1	13 1	NP1_LYMST
8	23	26.7	13 1	NP2_LYMST
9	22	25.6	13 1	NP3_LYMST
10	21	24.4	13 1	NP4_LYMST
11	21	24.4	13 1	PSBP_PINPS
12	21	24.4	15 1	ECDA_LYMST
13	19	22.1	12 1	NUDM_CANFA
14	19	22.1	13 1	NP5_LYMST
15	19	22.1	14 1	MY14_EISFO
16	19	22.1	15 1	UC14_MAIZE
17	19	22.1	16 1	ARCD_PSEPU
18	18	20.9	7 1	UN06_PINPS
19	18	20.9	12 1	PSP3_PHYPA
20	18	20.9	12 1	RS19_ELYEP
21	18	20.9	12 1	RS19_ELYEP
22	18	20.9	14 1	ADFA_TENMO
23	18	20.9	14 1	RS19_CLOPP
24	18	20.9	14 1	RS19_LOWBP
25	18	20.9	15 1	ACT_PINPS
26	18	20.9	15 1	FIBA_ANAPL
27	18	20.9	15 1	UC19_MAIZE
28	18	20.9	16 1	ALRX_PSEPU
29	18	20.9	16 1	MLB_SQUAC
30	18	20.9	16 1	RIPK_TRITCI
31	18	20.9	16 1	SAL3_ONCMY
32	17	19.8	14 1	TKN1_SCHRG
33	17	19.8	15 1	RS10_BACST

34	17	19.8	15 1	SAL1_ONCMY	P81369 oncorhynch
35	17	19.8	15 1	SODM_ENTAE	P22799 enterobacte
36	17	19.8	15 1	UC23_MAIZE	P80629 zea mays (m
37	17	19.8	16 1	AL11_CALVO	P41839 bacillifera
38	17	19.8	16 1	PPAC_BACME	P56948 bacillus me
39	16	18.6	8 1	LSK1_LEUMA	P21140 leucophaea
40	16	18.6	8 1	NS3_MYCTU	P81152 mycobacteri
41	16	18.6	10 1	ABGL_AGRAR	P83465 agrocycbe ae
42	16	18.6	10 1	PAR2_PENMO	P83317 penaeus mon
43	16	18.6	10 1	RL16_ACHLA	P29221 acholeplasm
44	16	18.6	10 1	TKN1_SCYCA	P08608 scylliorhinu
45	16	18.6	11 1	CA32_LITCI	P82090 litorea cit

## ALIGNMENTS

RESULT 1	ID	NSK1_SARBU	STANDARD;	PRT;	9 AA.
AC	P41452;	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	Neosulfakinin-I (NEB-SK-I).				
OS	Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;				
OC	Sarcophagidae; Sarcophaga.				
OX	NCBI_TaxID=7385;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE-Head.				
RX	MEDLINE=93083101; PubMed=1360367;				
RA	Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;				
RT	"Isolation and primary structure of two sulfakinin-like peptides from				
RT	the fleshfly, Neobellieria bullata."				
RL	Comp. Biochem. Physiol. 103C:135-142(1992).				
CC	-1- FUNCTION: Myotropic peptide.				
CC	-1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.				
DR	InterPro; IPR001651; Gastrin.				
DR	PROSITE; PS00259; GASTRIN; 1.				
KW	Neuropeptide; Amidation; Sulfation.				
FT	MOD RES	4	4	SULFATION (POTENTIAL).	
FT	MOD RES	9	9	AMIDATION (POTENTIAL).	
SO	SEQUENCE	9 AA; 1187 MW; 880A0691586B5AAA CRC64;			
Query Match		39.5%;	Score 34; DB 1; Length 9;		
Best Local Similarity		55.6%;	Pred. No. 1.4e+05;		
Matches	5; Conservative	1; Mismatches	3; Indels	0; Gaps	0;
Qy	6 YDQYGHAAAF 14				
Db	1 PDDYGHMRF 9				
RESULT 2					
ID	LSKP_PERAM	STANDARD;	PRT;	11 AA.	
AC	P36885;				
DT	01-JUN-1994 (Rel. 29, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	01-FEB-1996 (Rel. 33, Last annotation update)				
DE	Perisulfakinin (Pea-SK-I).				
OS	Periplaneta americana (American cockroach).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;				
OC	Blattidae; Periplaneta.				
OX	NCBI_TaxID=6978;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Corpora cardiaca;				
RX	MEDLINE=90137190; PubMed=2615921;				

RA Veenstra J.A.;  
 RT "Isolation and structure of two gastrin/CCK-like neuropeptides from  
 RL the American cockroach homologous to the leucosulfakinins.";  
 CC Neuropeptides 14:145-149(1989).  
 CC -1- FUNCTION: Stimulates hindgut contractions.  
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR PIR; A60656; A60656.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KM Hormone; Amidation; Sulfation.  
 FT MOD\_RES 6  
 FT MOD\_RES 11  
 SQ SEQUENCE 11 AA; 1445 MW; 8B4E0680E86B5AAA CRC64;  
 Query Match 39.5%; Score 34; DB 1; Length 11;  
 Best Local Similarity 55.6%; Pred. No. 5;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 6 YDYGHAAP 14  
 DB 3 FDDYGHMRF 11  
 RESULT 3  
 MSK2\_SARBU STANDARD; PRT; 14 AA.  
 ID MSK2\_SARBU  
 AC P41493;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE Neosulfakinin-II (NEB-SK-II).  
 OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;  
 CC Sarcophagidae; Sarcophaga.  
 OC NCBI\_TaxID=7385;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Head;  
 RX MEDLINE=93083101; PubMed=1360367;  
 RA Fonagy A., Schoofs L., Proost P., van Damme J., de Loof A.;  
 RT "Isolation and primary structure of two sulfakinin-like peptides from  
 RL the fleshfly, Neobellieria bullata.";  
 RL Comp. Biochem. Physiol. 103C:135-142(1992).  
 CC -1- FUNCTION: Myotropic peptide.  
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 CC PIR; A56632; A56632.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KM Neuropeptide; Amidation; Sulfation.  
 FT MOD\_RES 9  
 FT MOD\_RES 14  
 SQ SEQUENCE 14 AA; 1794 MW; 8B4E06D5B61C62AA CRC64;  
 Query Match 39.5%; Score 34; DB 1; Length 14;  
 Best Local Similarity 55.6%; Pred. No. 6.5;  
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 6 YDYGHAAP 14  
 DB 6 FDDYGHMRF 14  
 RESULT 4  
 LSK2\_LOCM1 STANDARD; PRT; 12 AA.  
 ID LSK2\_LOCM1  
 AC P47733;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Sulfakinin (LOM-SK).  
 OS Locusta migratoria (Migratory locust).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;  
 OC Acridoidea; Acrididae; Oedipodinae; Locusta.  
 OC NCBI\_TaxID=7004;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Brain;  
 RA Schoofs L., Holman G.L., Hayes T.K., Nachman R.J., de Loof A.;  
 RL (in) McCaffery A., Wilson I. (eds.);  
 RL Chromatography and isolation of insect hormones and pheromones,  
 RL pp.231-241, Plenum Press, New York (1990).  
 CC -1- FUNCTION: Myotropic peptide.  
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KM Hormone; Amidation; Sulfation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1  
 FT MOD\_RES 7  
 FT MOD\_RES 12  
 FT MOD\_RES 12  
 SQ SEQUENCE 12 AA; 1440 MW; 9B5BDA9BD5B5AAA CRC64;  
 Query Match 38.4%; Score 33; DB 1; Length 12;  
 Best Local Similarity 60.0%; Pred. No. 8.2;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 5 AYDYGHAAP 14  
 DB 3 ASDYGHMRF 12  
 RESULT 5  
 LSK2\_LEUMA STANDARD; PRT; 10 AA.  
 ID LSK2\_LEUMA  
 AC P09039;  
 DT 01-NOV-1988 (Rel. 09, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Leucosulfakinin-II (LSK-II).  
 OS Leucophaea maderae (Madeira cockroach), and  
 OS Periplaneta americana (American cockroach).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;  
 OC Blaberidae; Leucophaea.  
 OC NCBI\_TaxID=6968, 6978;  
 RN [1]  
 RP SEQUENCE.  
 RC SPECIES=L. maderae;  
 RX MEDLINE=87048769; PubMed=3778455;  
 RA Nachman R.J., Holman G.M., Cook B.J., Haddon W.F., Ling N.;  
 RT "Leucosulfakinin-II, a blocked sulfated insect neuropeptide with  
 RL homology to cholecystokinin and gastrin.";  
 RL Biochem. Biophys. Res. Commun. 140:357-364(1986).  
 RN [2]  
 RP SEQUENCE.  
 RC SPECIES=P. americana; TISSUE=Corpora cardiaca;  
 RX MEDLINE=90137190; PubMed=2615921;  
 RA Veenstra J.A.;  
 RT "Isolation and structure of two gastrin/CCK-like neuropeptides from  
 RL the American cockroach homologous to the leucosulfakinins.";  
 RL Neuropeptides 14:145-149(1989).  
 CC -1- FUNCTION: CHANGE THE FREQUENCY AND AMPLITUDE OF CONTRACTIONS OF  
 CC THE COCKROACH HINGUT. STIMULATES MUSCLE CONTRACTION OF HINGUT.  
 CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.  
 CC PIR; A26335; GMR0L2.  
 DR PIR; B60656; B60656.  
 DR InterPro; IPR001651; Gastrin.  
 DR PROSITE; PS00259; GASTRIN; 1.  
 KM Hormone; Amidation; Sulfation; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1  
 FT MOD\_RES 5  
 FT MOD\_RES 1  
 FT MOD\_RES 1  
 SQ SEQUENCE 10 AA; 1255 MW; 9B4F531E86B5AAA CRC64;



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:33:34 ; Search time 52 Seconds  
(without alignments)  
86.938 Million cell updates/sec

Title: US-10-001-938-3  
Perfect score: 86  
Sequence: 1 GKRAAYDQYGHAAFEQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 459173

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_290Jan04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	86	100.0	16	5	AU98852
2	86	100.0	16	6	ABR55126
3	81	94.2	15	2	AAW25795
4	81	94.2	15	3	AAV79543
5	81	94.2	15	4	AAW99341
6	81	94.2	15	5	AAU09842
7	81	94.2	15	5	AAU98876
8	81	94.2	15	5	AAE19457
9	81	94.2	15	6	ABR55132
10	81	94.2	15	6	AAW99344
11	72	83.7	15	2	AAW95446
12	72	83.7	15	2	AAW25796
13	72	83.7	15	5	AAE19458
14	72	83.7	15	6	ABR55133
15	64.5	75.0	14	2	AAW95445
16	54	62.8	15	2	AAW25798
17	54	62.8	15	6	ABR55123
18	34	39.5	9	4	AAU03347
19	34	39.5	9	4	AAU03346
20	34	39.5	9	4	AAU03351
21	34	39.5	9	7	ADE14680
22	34	39.5	9	7	ADE14676
23	34	39.5	9	7	ADE14679
24	34	39.5	9	7	ADE14677
25	34	39.5	14	3	ABR14081

26	34	39.5	14	4	AAU03353	AAU03353	Fruit fly
27	34	39.5	14	6	AAW9793	AAW9793	Peptide 6
28	34	39.5	14	7	ABR14681	ABR14681	Drosulfak
29	34	39.5	15	2	AAW10086	AAW10086	HLA DW4 1
30	34	39.5	15	2	AAW10089	AAW10089	HLA DW4
31	34	39.5	15	2	AAW25799	AAW25799	Synthetic
32	34	39.5	15	2	AAW25800	AAW25800	Synthetic
33	34	39.5	15	3	AAW9544	AAW9544	Human leu
34	34	39.5	15	3	AAW99340	AAW99340	Vaccine r
35	34	39.5	15	5	AAW09843	AAW09843	Human leu
36	34	39.5	15	6	ABR55138	ABR55138	Human S1
37	34	39.5	15	6	ABR55139	ABR55139	Human S2
38	34	39.5	15	6	AAW79792	AAW79792	Peptide 6
39	31	36.0	12	3	AAW40050	AAW40050	Anti-htl1
40	31	36.0	12	3	AAW39771	AAW39771	Anti-TIL2
41	31	36.0	12	3	AAW39769	AAW39769	Anti-TIL2
42	31	36.0	12	3	AAW39510	AAW39510	Anti-htl-
43	31	36.0	14	3	ABR13800	ABR13800	Human HLA
44	31	36.0	14	3	ABR14089	ABR14089	Human HLA
45	31	36.0	14	6	AAW79798	AAW79798	Peptide 6

## ALIGNMENTS

RESULT 1	AAU98852	standard; peptide; 16 AA.
ID	AAU98852	standard; peptide; 16 AA.
AC	AAU98852;	
DT	22-AUG-2002	(first entry)
XX		
DB	E.Coli DNAI 61 immunogenic peptide.	
XX		
KM	Immunogenic peptide; heat shock protein; HSP; DNAI; immunomodulatory;	
KW	cytotoxic; antiinflammatory; antibacterial; antitubercular;	
KW	autoimmune disease; arthritis; articular juvenile idiopathic arthritis;	
KW	infectious disease; inflammatory bowel disease; cancer;	
KW	mucosal toleration; DNA vaccination; energy induction.	
XX		
OS	Escherichia coli.	
XX		
PN	WO200236611-A2.	
XX		
PD	10-MAY-2002.	
XX		
PF	31-OCT-2001; 2001WO-US045344.	
XX		
PR	01-NOV-2000; 2000US-0245181P.	
XX		
PA	(REGC ) UNIV CALIFORNIA.	
XX	(MART/) MARTINI A.	
XX		
PI	Martini A, Albani S, Carson DA, Prekren BJ;	
XX	WPI, 2002-489999/52.	
XX		
PT	New immunomodulatory peptides from heat shock proteins, useful for	
PT	treating immunological disorder in subjects such as humans, e.g.	
PT	autoimmune disease (e.g. arthritis), infectious disease, inflammatory	
PT	bowel disease or cancer.	
XX		
PS	Claim 4, Page 55, 84pp; English.	
XX		
CC	This invention relates to the use of a peptide, which is an immunogenic	
CC	portion derived from a dna heat shock protein (hsp) in modulating an	
CC	immune response in a subject. The peptides of the invention may have	
CC	immunomodulatory, cytostatic, antiinflammatory, antibacterial or	
CC	antitubercular properties and can stimulate expression of interleukins,	
CC	tumour necrosis factor and transforming growth factor beta. The	
CC	immunogenic peptide is useful for modulating (i.e. augmenting/inducing or	
CC	reducing/inhibiting) an immune response in a subject having an	

immunological disorder (e.g. autoimmune disease such as arthritis or  
arthritis juvenile idiopathic arthritis), an infectious disease, an  
inflammatory bowel disease or cancer. The immunogenic peptide of the  
invention is also useful for modulating immunoreceptor cell  
responsiveness in a subject. The immunogenic peptide is particularly  
useful for treating the above-mentioned diseases in mammals, e.g. cat,  
dog, horse, farm animal (e.g. ovine, bovine or porcine) or human. In  
general, the peptide is useful in methods involving mucosal toleration,  
DNA vaccination, allergy induction or active immunisation. The present  
sequence represents an E. coli DNA immunogenic peptide of the invention

Query March 100.0%; Score 86; DB 5; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDYGHAPEQ 16  
DB 1 QKRAAYDYGHAPEQ 16

RESULT 2  
ABRS5126 standard; peptide; 16 AA.  
ID ABR55126;  
AC ABR55126;  
XX  
XX  
XX 03-JUL-2003 (first entry)  
DE  
E. coli dnaJ1 antigen-specific epitope peptide.  
XX  
XX Antigen-specific epitope; immune response; T cell; cytokine;  
XX antiarthritic; antidiabetic; neuroprotective; anti-inflammatory;  
XX cyclosporatic; antihypertensive; immunosuppressive;  
XX antiproliferative; anti-ulcer; antianemic; cardiac; respiratory;  
XX antiallergic; dermatological; antipsoriatic.  
XX  
XX Escherichia coli.  
XX  
XX WO2003026579-A2.  
XX  
XX 03-APR-2003.  
XX  
XX 25-SEP-2002; 2002WO-US030578.  
XX  
XX 25-SEP-2001; 2001US-0325499P.  
XX  
XX 11-DEC-2001; 2001US-0339284P.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Alpani S, Martins A;  
XX  
XX WPI; 2003-430097/40.  
XX  
XX  
XX Modulating an immune response in a subject having an immune-related  
PT disorder, e.g. arthritis by administering an antigen-specific epitope and  
PT a cytokine or an agent that effects cytokine activity or expression.  
XX  
XX  
XX Disclosure; Page 9; 41pp; English.

The invention relates to a novel method for modulating an immune response  
in a subject having an immune-related disorder. The method comprises: (a)  
administering an antigen-specific epitope, where administration provides  
an epitope-specific T cell immune modulation; and (b) administering a  
cytokine, an agent that effects cytokine activity or expression, or an  
anticytokine therapy. The method of the invention has antiarthritic,  
antidiabetic, neuroprotective, anti-inflammatory, cyclosporatic,  
antihypertensive, anti-ulcer, antianemic, immunosuppressive, antipsoriatic,  
antiallergic, cardiac, respiratory, antiproliferative, antiproliferative,  
ulcer, antianemic, cardiac, respiratory, antiproliferative, antiproliferative,  
dermatological, and antipsoriatic activity. The method is useful for  
modulating an immune response in a subject having an immune-related  
disorder. The present sequence is used in the exemplification of the

invention

QY Sequence 16 AA;  
SQ

Query Match 100.0%; Score 86; DB 6; Length 16;  
Best Local Similarity 100.0%; Pred. No. 4.1e-08;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDYGHAPEQ 16  
DB 1 QKRAAYDYGHAPEQ 16

RESULT 3  
AAW25795 standard; peptide; 15 AA.  
ID AAW25795;  
AC AAW25795;  
XX  
XX 06-APR-1998 (first entry)  
DE  
Peptide dnaJ1 which protects against arthritogenic peptides.  
XX  
XX dnaJ protein; dnaJ1; adult rheumatoid arthritis; vaccine;  
XX arthritogenic peptide; autoimmune disease; systemic immune system;  
XX anti-dnaJ1 antibody; passive immunisation;  
XX rheumatoid arthritis-susceptibility detection.  
XX  
XX Escherichia coli.  
XX  
XX WO9734002-A1.  
XX  
XX 18-SEP-1997.  
XX  
XX 20-FEB-1997; 97WO-US002957.  
XX  
XX 15-MAR-1996; 96US-00618464.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Carson DA, Alpani S;  
XX  
XX WPI; 1997-470882/43.  
XX  
XX  
XX Vaccine for protecting against arthritogenic peptide(s) containing dnaJ1  
PT - also determining pre-disposition to rheumatoid arthritis by detecting  
PT anti-arthritogenic peptide antibodies.  
XX  
XX  
XX Disclosure; Page 5; 44pp; English.

Peptides AAW25795-96 and AAW25798 are derived from the dnaJ protein from  
Escherichia coli. One peptide, dnaJ1 (AAW25795) was found to induce  
relatively strong immune response in seropositive adult rheumatoid  
arthritis patients. This peptide was used in a vaccine for protecting  
against arthritogenic peptides. The vaccine contains a carrier, pure  
dnaJ1 peptide or a recombinant gene expression vector encoding the  
dnaJ1 peptide. The vaccines are used to prevent rheumatoid arthritis (or  
other autoimmune diseases). Vaccines can target the arthritogenic  
peptides before they are presented to the systemic immune system. Anti-  
dnaJ1 antibodies can also be used for passive immunisation. Antibodies  
can be used to detect rheumatoid arthritis-susceptibility sequences on  
HLA or in populations of E. coli in the gastrointestinal tract

Query Match 94.2%; Score 81; DB 2; Length 15;  
Best Local Similarity 100.0%; Pred. No. 2.9e-07;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QKRAAYDYGHAPE 15  
DB 1 QKRAAYDYGHAPE 15



082404  
ID 082404 PRELIMINARY; PRT; 16 AA.  
AC 082404;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).  
GN ADH.  
OS *Fragaria nilgerrensis*.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids I; Rosales; Rosaceae; Rosoideae; Fragaria.  
OX NCBI\_TaxID=64941;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=Berlin 1;  
RA Yu H., Davis T.M.;  
RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF000217; AAC3654.1; -;  
DR GO: GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.  
DR GO: GO:0004023; F:alcohol dehydrogenase activity, metal ion-i...; IEA.  
DR GO: GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
KW Oxidoreductase.  
FT NON\_TER 1 1  
FT SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;  
SQ

Query Match 27.9%; Score 24; DB 10; Length 16;  
Best Local Similarity 80.0%; Pred. No. 2.9e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 YGHA 13  
Db 10 YGHA 14

RESULT 3  
082406 PRELIMINARY; PRT; 16 AA.  
ID 082406;  
AC 082406;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).  
GN ADH.  
OS *Fragaria moschata*.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids I; Rosales; Rosaceae; Rosoideae; Fragaria.  
OX NCBI\_TaxID=64940;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=FRA 157;  
RA Yu H., Davis T.M.;  
RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF000219; AAC3654.1; -;  
DR GO: GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.  
DR GO: GO:0004023; F:alcohol dehydrogenase activity, metal ion-i...; IEA.  
DR GO: GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
KW Oxidoreductase.  
FT NON\_TER 1 1  
FT SEQUENCE 16 AA; 1713 MW; CEF73B5B28A4D952 CRC64;  
SQ

Query Match 27.9%; Score 24; DB 10; Length 16;  
Best Local Similarity 80.0%; Pred. No. 2.9e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 YGHA 13  
Db 10 YGHA 14

Query Match 27.9%; Score 24; DB 10; Length 16;  
Best Local Similarity 80.0%; Pred. No. 2.9e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 4  
082402 PRELIMINARY; PRT; 16 AA.  
ID 082402;  
AC 082402;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Alcohol dehydrogenase (EC 1.1.1.1) (Fragment).  
GN ADH.  
OS *Fragaria nubicola*.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids I; Rosales; Rosaceae; Rosoideae; Fragaria.  
OX NCBI\_TaxID=60188;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=FRA520;  
RA Yu H., Davis T.M.;  
RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF000213; AAC3654.0.1; -;  
DR GO: GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.  
DR GO: GO:0004023; F:alcohol dehydrogenase activity, metal ion-i...; IEA.  
DR GO: GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
KW Oxidoreductase.  
FT NON\_TER 1 1  
FT SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;  
SQ

Query Match 27.9%; Score 24; DB 10; Length 16;  
Best Local Similarity 80.0%; Pred. No. 2.9e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 YGHA 13  
Db 10 YGHA 14

RESULT 5  
082781 PRELIMINARY; PRT; 16 AA.  
ID 082781;  
AC 082781;  
DT 01-NOV-1998 (TREMBlrel. 08, Created)  
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Alcohol dehydrogenase (EC 1.1.1.1) (Aldehyde reductase) (Fragment).  
GN ADH.  
OS *Fragaria vesca* (Woodland strawberry).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
OC eucosids I; Rosales; Rosaceae; Rosoideae; Fragaria.  
OX NCBI\_TaxID=57918;  
RN (1)  
RP SEQUENCE FROM N.A.  
RC STRAIN=YELLOW WONDER, and BARON SOLEWACHER;  
RA Yu H., Davis T.M.;  
RL "Genetic relationships among *Fragaria* species based on RAPDs and an alcohol dehydrogenase (ADH) gene.";  
RT Genome 0:0-0(1997).  
CC -1- CATALYTIC ACTIVITY: AN ALCOHOL + NAD(+) = AN ALDEHYDE OR KETONE + NADH.  
CC -1- Cofactor: ZINC OR IRON.  
CC EMBL: AF000216; AAC3654.1; -;  
CC EMBL: AF000214; AAC3654.1; -;  
DR GO: GO:0004025; F:alcohol dehydrogenase activity, iron-dependent; IEA.  
DR GO: GO:0004023; F:alcohol dehydrogenase activity, metal ion-i...; IEA.  
DR GO: GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.  
DR GO: GO:0016491; F:oxidoreductase activity; IEA.  
KW Oxidoreductase.  
FT NON\_TER 1 1  
FT SEQUENCE 16 AA; 1682 MW; CEF73B5B28A4D817 CRC64;  
SQ

Query Match 27.9%; Score 24; DB 10; Length 16;  
Best Local Similarity 80.0%; Pred. No. 2.9e+03;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 11, 2004, 09:37:59 ; Search time 23 Seconds

(without alignments)  
35.914 Million cell updates/sec

Title: US-10-001-938-3

Sequence: 1 QKRAHYDQYGHAAFEQ 16

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 152138

Minimum DB seq length: 0  
Maximum DB seq length: 16

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep:\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep:\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/2/1aa/6C\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/2/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	81	94.2	15	1	US-08-618-464-4	Sequence 4, Appl1
2	81	94.2	15	3	US-09-107-615-4	Sequence 4, Appl1
3	81	94.2	15	5	PCT-US95-04896-4	Sequence 4, Appl1
4	72	83.7	15	1	US-08-618-464-5	Sequence 5, Appl1
5	72	83.7	15	3	US-09-107-615-5	Sequence 5, Appl1
6	72	83.7	15	5	PCT-US95-04896-5	Sequence 5, Appl1
7	54	62.8	15	1	US-08-618-464-6	Sequence 6, Appl1
8	54	62.8	15	3	US-09-107-615-6	Sequence 6, Appl1
9	34	39.5	15	1	US-08-618-464-7	Sequence 7, Appl1
10	34	39.5	15	3	US-09-107-615-7	Sequence 7, Appl1
11	34	39.5	15	5	US-08-618-464-8	Sequence 8, Appl1
12	31	36.0	12	1	US-07-732-114A-5	Sequence 5, Appl1
13	31	36.0	12	1	US-08-170-114A-5	Sequence 5, Appl1
14	31	36.0	14	2	US-08-323-686-3	Sequence 3, Appl1
15	31	36.0	14	2	US-08-323-686-6	Sequence 3, Appl1
16	31	36.0	14	4	US-09-255-501-67	Sequence 26, Appl1
17	31	36.0	14	4	US-09-255-501-67	Sequence 67, Appl1
18	31	36.0	14	4	US-09-255-501-68	Sequence 68, Appl1
19	30	34.9	9	4	US-09-721-870-180	Sequence 180, App
20	30	34.9	15	3	US-08-467-023-255	Sequence 255, App
21	28	32.6	11	3	US-08-467-580-14	Sequence 14, Appl1
22	28	32.6	11	5	PCT-US95-08516-14	Sequence 14, Appl1
23	28	32.6	15	2	US-08-521-871A-3	Sequence 3, Appl1
24	27	31.4	12	1	US-07-732-114A-11	Sequence 11, Appl1
25	27	31.4	12	1	US-08-170-114A-11	Sequence 11, Appl1
26	27	31.4	13	1	US-08-487-568-45	Sequence 45, Appl1
27	26	30.2	6	1	US-07-995-503A-12	Sequence 12, Appl1

28	26	30.2	6	1	US-08-390-510-12	Sequence 12, Appl1
29	26	30.2	6	1	US-08-390-790-12	Sequence 12, Appl1
30	26	30.2	6	2	US-08-390-509-12	Sequence 12, Appl1
31	26	30.2	6	3	US-09-149-860A-12	Sequence 12, Appl1
32	26	30.2	12	1	US-07-995-503A-11	Sequence 11, Appl1
33	26	30.2	12	1	US-08-390-510-11	Sequence 11, Appl1
34	26	30.2	12	1	US-08-390-790-11	Sequence 11, Appl1
35	26	30.2	12	2	US-08-390-509-11	Sequence 11, Appl1
36	26	30.2	12	2	US-08-149-860A-11	Sequence 11, Appl1
37	26	30.2	13	2	US-08-194-981E-8	Sequence 8, Appl1
38	26	30.2	15	2	US-08-521-871A-4	Sequence 8, Appl1
39	26	30.2	15	3	US-09-613-182-1	Sequence 1, Appl1
40	26	30.2	15	4	US-09-490-702B-19	Sequence 19, Appl1
41	26	30.2	15	4	US-09-490-702B-96	Sequence 96, Appl1
42	26	30.2	15	4	US-09-255-501-69	Sequence 69, Appl1
43	26	30.2	16	3	US-09-181-896-2	Sequence 2, Appl1
44	26	30.2	16	4	US-09-490-702B-95	Sequence 95, Appl1
45	25	29.1	9	1	US-08-186-266-11	Sequence 11, Appl1

## ALIGNMENTS

RESULT 1  
US-08-618-464-4  
Sequence 4, Application US/08618464  
Patent No. 5773570  
GENERAL INFORMATION:  
APPLICANT: CARSON, DENNIS A.  
APPLICANT: ALBANI, SALVATORE  
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN  
IMMUNE PROTECTION AGAINST ARTHRITIS  
TITLE OF INVENTION: INVOLVED IN  
TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: FISH & RICHARDSON P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/618,464  
FILING DATE:  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: HOWELLS, STACY L.  
REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: 07340/042001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070  
TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
CLONE: Immunogenic clau Peptide  
FEATURES:  
NAME/KEY: Peptide  
LOCATION: 1..15  
US-08-618-464-4  
Query Match 94.2% ; Score 81; DB 1; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDYGHAPE 15  
Db 1 OKRAAYDYGHAPE 15

RESULT 2  
US-09-107-615-4

Sequence 4, Application US/09107615  
Patent No. 6153200

GENERAL INFORMATION:  
APPLICANT: CARSON, DENNIS A.  
APPLICANT: ALBANI, SALVATORE  
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN  
INDUCING IMMUNE PROTECTION AGAINST  
TITLE OF INVENTION: ARTHROGENIC PEPTIDES INVOLVED IN  
TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FISH & RICHARDSON P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,615

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/618,464

FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: HOWELLS, STACY L.

REGISTRATION NUMBER: 34,842  
REFERENCE/DOCKET NUMBER: 07340/042001

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099  
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids

TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide

IMMEDIATE SOURCE:  
CLONE: Immunogenic dna Peptide

FEATURE:  
NAME/KEY: Peptide

LOCATION: 1..15  
US-09-107-615-4

Query Match 94.2%; Score 81; DB 3; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDYGHAPE 15  
Db 1 OKRAAYDYGHAPE 15

RESULT 3  
PCT-US95-04896-4

Sequence 4, Application PC/TUS9504896  
GENERAL INFORMATION:

APPLICANT: THE REGENTS OF THE UNIVERSITY  
APPLICANT: OF CALIFORNIA  
TITLE OF INVENTION: METHOD AND REAGENTS FOR THE TREATMENT  
TITLE OF INVENTION: OF RHEUMATOID ARTHRITIS  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ROBBINS, BERLINER & CARSON  
STREET: 201 N. FIGUEROA STREET, 5TH FLOOR  
CITY: LOS ANGELES  
STATE: CALIFORNIA  
COUNTRY: US  
ZIP: 90012

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04896

FILING DATE:  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: BERLINER, ROBERT

REGISTRATION NUMBER: 20,121  
REFERENCE/DOCKET NUMBER: 5555-314

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213-977-1001

TELEFAX: 213-977-1003  
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 15 amino acids

TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide

IMMEDIATE SOURCE:  
CLONE: Immunogenic dna Peptide

FEATURE:  
NAME/KEY: Peptide

LOCATION: 1..15  
PCT-US95-04896-4

Query Match 94.2%; Score 81; DB 5; Length 15;  
Best Local Similarity 100.0%; Pred. No. 5.8e-08;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 OKRAAYDYGHAPE 15  
Db 1 OKRAAYDYGHAPE 15

RESULT 4  
US-08-618-464-5

Sequence 5, Application US/08618464  
Patent No. 5773570

GENERAL INFORMATION:  
APPLICANT: CARSON, DENNIS A.

APPLICANT: ALBANI, SALVATORE  
TITLE OF INVENTION: VACCINE COMPOSITIONS AND METHODS USEFUL IN

INDUCING IMMUNE PROTECTION AGAINST ARTHRITIS  
TITLE OF INVENTION: INVOLVED IN  
TITLE OF INVENTION: THE PATHOGENESIS OF RHEUMATOID ARTHRITIS

NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:

ADDRESSEE: FISH & RICHARDSON P.C.  
STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla  
STATE: CALIFORNIA

COUNTRY: US  
ZIP: 92037

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible